SUPPORT FOR THE AMENDMENTS

The amendments to Claims 1, 3, 4, 8, 11, and 12, and newly added Claims 40-52 are supported by the specification at pages 2-27. Support for the new Sequence Listing is found in on page 1, lines 5-8, which incorporates the priority document by reference. No new matter is believed to have been added to this application by these amendments.

REMARKS

Claims 1-4, 8-9, 11-13, 20-36, and 39-52 are pending. Favorable reconsideration is respectfully requested.

Applicants have now submitted a substitute Sequence Listing and a corresponding computer-readable Sequence Listing. The sequence information recorded in the corresponding computer-readable Sequence Listing is identical to the paper copy of the substitute Sequence Listing. Support for all of the sequences listed in the substitute Sequence Listing is found in the present application as originally filed. No new matter is believed to have been introduced by the submission of the substitute Sequence Listing and the corresponding computer-readable Sequence Listing.

The rejection under 35 U.S.C. §112, first paragraph, is believed to be obviated by the amendment submitted above. The claims discussed in the rejection have been canceled. Accordingly, withdrawal of this ground of rejection is respectfully requested.

The rejection under 35 U.S.C. §112, second paragraph, is believed to be obviated by the amendment submitted above in part and is, in part, respectfully traversed.

Applicants submit that the substitute Sequence Listing corrects the issues with respect to Claims 1-19 and 37-38.

Claims 5-7 have been canceled.

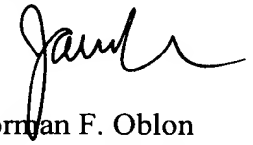
Regarding Claims 2 and 9, the present specification provides a detailed description that the claimed polynucleotide encodes a protein which regulates transcription of the LysR1 gene. See, for example, the text bridging pages 2 and 3. In view of this detailed description, one skilled in the art will readily appreciate the meaning of these claims.

Based on the foregoing, the claims are definite within the meaning of 35 U.S.C. §112, second paragraph. Accordingly, withdrawal of this ground of rejection is respectfully requested.

Applicants submit that the application is in condition for allowance. Early notice to this effect is earnestly solicited.

Respectfully submitted,

OBLON, SPIVAK, McCLELLAND,
MAIER & NEUSTADT, P.C.



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Serial No.: 09/903,770
Amendment Filed On: HEREWITH

IN THE SPECIFICATION

Please amend the specification as follows:

Page 33 (Abstract of the Disclosure), please replace the Sequence Listing filed on July 13, 2001 with the attached substitute Sequence Listing.

IN THE CLAIMS

--1. (Amended) An isolated polynucleotide from *Corynebacterium* which encodes a protein comprising the amino acid sequence of SEQ ID NO:3 [2].

2. The isolated polynucleotide of Claim 1, wherein said protein has LysR1 transcriptional reguatory activity.

3. (Amended) An isolated polynucleotide, which comprises nucleotides 201 to 1109 of SEQ ID NO:1 and degenerates thereof.

4. (Amended) An isolated polynucleotide, which comprises the full complement of polynucleotide of SEQ ID NO: 1 nucleotides 201 to 1109 [which is complimentary to the polynucleotide of Claim 3].

8. (Amended) An isolated polynucleotide from *Corynebacterium glutamicum* which hybridizes under stringent conditions to the polynucleotide of Claim 3; wherein said stringent conditions comprise washing in 5X SSC at a temperature from 50 to 68°C.

9. The isolated polynucleotide of Claim 3, which encodes a protein having LysR1 transcriptional regulatory activity.

11. (Amended) An [The] isolated polynucleotide consisting of 15 to 383 consecutive nucleotides selected from SEQ ID NO: 1 [of Claim 10 which comprises SEQ ID NO:3].

12. A vector comprising the isolated polynucleotide of Claim 1.

13. A vector comprising the isolated polynucleotide of Claim 3.

20. A *Coryneform* bacterium which comprises an attenuated lysR1 gene.

21. (Amended) The *Coryneform* bacterium of Claim 20 [21], wherein said lysR1 gene comprises the polynucleotide sequence of SEQ ID NO:1.

22. *Escherichia Coli* DSM 13616.

23. A process for producing L-amino acids comprising culturing a bacterial cell in a medium suitable for producing L-amino acids, wherein said bacterial cell comprises an attenuated lysR1 gene.

24. The process of Claim 23, wherein said bacterial cell is a *Coryneform bacterium or Brevibacterim.*

25. The process of Claim 24, wherein said bacterial cell is selected from the group consisting of *Coryneform glutamicum, Corynebacterium acetoglutamicum, Corynebacterium acetoacidophilum, Corynebacterium melassecola, Corynebacterium thermoaminogenes, Brevibacterium flavum, Brevibacterium lactofermentum, Brevibacterium divaricatum.*

26. The process of Claim 23, wherien said lysR1 gene comprisies the polynucleoitde sequence of SEQ ID NO:1.

27. The process of Claim 23, wherein said L-amino acid is L-lysine.

28. The process of Claim 23, wherein said L-amino acid is L-valine.

29. The process of Claim 23, wherein said bacteria further comprises at least one gene whose expression is enhanced, wherein said gene is selected from the group consisting of dapA, eno, zwf, pyc, and lysE.

30. The process of Claim 23, wherein said bacteria further comprises at least one gene whose expression is attenuated, wherein said gene is selected from the group consisting of pck, pgi, and poxB.

31. A process for screening for polynucleotides which encode a protein having LysR1 transcriptional regulatory activity comprising hybridizing the isolated polynucleotide of Claim 1 to the polynucleotide to be screened; expressing the polynucleotide to produce a protein; and detecting the presence or absence of LysR1 transcriptional regulatory activity in said protein.

32. A process for screening for polynucleotides which encode a protein having LysR1 transcriptional regulatory activity comprising hybridizing the isolated polynucleotide of Claim 3 to the polynucleotide to be screened; expressing the polynucleotide to produce a protein; and detecting the presence or absence of LysR1 transcriptional regulatory activity in said protein.

33. A method for detecting a nucleic acid with at least 70% homology to nucleotide of Claim 1, comprising contacting a nucleic acid sample with a probe or primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 1, or at least 15 consecutive nucleotides of the complement thereof.

34. A method for producing a nucleic acid with at least 70% homology to nucleotide of Claim 1, comprising contacting a nucleic acid sample with a primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 1, or at least 15 consecutive nucleotides of the complement thereof.

35. A method for detecting a nucleic acid with at least 70% homology to nucleotide of Claim 3, comprising contacting a nucleic acid sample with a probe or primer comprising at

least 15 consecutive nucleotides of the nucleotide sequence of Claim 3, or at least 15 consecutive nucleotides of the complement thereof.

36. A method for producing a nucleic acid with at least 70% homology to nucleotide of Claim 3, comprising contacting a nucleic acid sample with a primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 3, or at least 15 consecutive nucleotides of the complement thereof.

39. An isolated polypeptide comprising the amino acid sequence of SEQ ID NO:2.--

Claims 40-52 (New)

SEQUENCE LISTING

<110> MOECKEL, BETTINA
FARWICK, MIKE
HERMANN, THOMAS
KREUTZER, CAROLINE
PFEFFERLE, WALTER

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